94. The isolated nucleic acid of claim 93, wherein said nucleic acid is up to 1,000 basepairs in length.

95. A method of identifying a cancer type, comprising determining a pattern of homozygous deletions in the methylthioadenosine phosphorylase gene on human chromosome 9p21, and associating said pattern with the pattern obtained from the particular cancer sought to be identified.

96. The method of claim 95, wherein said cancer is identified as a tumor cell, a leukemia, a glioma, a melanoma, bladder cancer, brain cancer, breast cancer, lung cancer, ovarian cancer, or pancreatic cancer.

REMARKS

Status of the Claims

Claims 1,7,8, 10-25, 34, 35 and 37 have been canceled. Claims 39-96 are pending in the case.

Rejection of Claims 1,7,8,10-25, 34, 35 and 37 under 35 U.S.C. section 102(b)

Claims 1,7,8,10-25, 34, 35 and 37 were rejected under 35 U.S.C. 102(b) as anticipated by the Kamb, et al, Bohlander et al and Nobori et al references which are asserted to disclose a larger nucleic acid segment containing the sequence of SEQ ID NO:1. Attention is directed to the new claims which are directed more particularly to SEQ ID NO:1. Claims 61-66 are directed to segments of the new gene having SEQ ID NO:1 and to segments that specifically hybridize to those segments under high stringency conditions. The specification on page 89 refers to high

stringency conditions. It is recognized in the art that high stringency conditions tolerate little if any mismatch so that the hybridized segments are almost completely complementary.

Applicant submits that the disclosed nucleic acid segment of SEQ ID NO:1 is not taught in any of the cited references, as previously discussed in applicant's response to office action, mailed 17 February 1998.

Nobori, *et al* is concerned with methylthioadenosine phosphorylase, an enzyme, not a nucleic acid. The focus of the reference is on immunoblotting methods to screen human cell lines and tumors for deficiency in the protein (see col 2, page 1098, 3rd paragraph). The Bohlander *et al* reference describes clones that represent attempts to map the MTAP gene but were not successful. The MTAP position was not determined; indeed, the clone was extremely large, on the order of 6.8 cM. There is some mention in the Bohlander reference to the Kamb *et al* work describing a tumor suppressor gene that is within $\pm$ 30 kb of some unknown gene. This is a vague and at best only an invitation to experiment (page 215, col 2) in an attempt isolation and characterization of new genes.. Kamb, et al. note that there are multiple genes in the 9p21 region (page 437, col 1, second paragraph). They describe a <u>putative</u> cell cycle regulator localized to a region on the order of 40 kb, again a large region with no indication of the location of the MTAP gene. Indeed the area is indicated to possibly include several genes. Such information provides less than complete guidance to isolate and identify an MTAP gene.

Applicant believes that the added claims fully and particularly define the MTAP gene and are responsive to the action's previous rejection as set forth in the advisory action. It is submitted that the application is in condition for allowance and reconsideration is respectfully requested.

Applicant intends this to be a complete response. Should any further issues remain, the undersigned attorney respectfully request a telephone call at 512-418-3108.

Respectfully submitted,

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Date: July 9, 1998